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OCT 03 2003

## RAW SEQUENCE LISTING

DATE: 09/30/2003

PATENT APPLICATION: US/09/759,990A

TIME: 10:27

Input Set : E:\31276-20026.00 - seqlist (final) fixed.txt

Output Set: N:\CRF4\09302003\I759990A.raw

3 <110> APPLICANT: AntiCancer, Inc.  
 4 Xu, Mingxu  
 5 Han, Qinghong  
 7 <120> TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH  
 8 SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE  
 9 (SAHH) AND IMPROVED ASSAYS FOR S-ADENOSYLMETHIONINE (SAM)  
 12 <130> FILE REFERENCE: 31276-20026.00  
 14 <140> CURRENT APPLICATION NUMBER: US 09/759,990A  
 15 <141> CURRENT FILING DATE: 2001-01-12  
 17 <150> PRIOR APPLICATION NUMBER: US 60/176,444  
 18 <151> PRIOR FILING DATE: 2000-01-14  
 20 <160> NUMBER OF SEQ ID NOS: 7  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1461  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens (nucleotide sequence of SAHH)  
 29 <400> SEQUENCE: 1

30 atggcttgca aatcacctac tgggtgctcca ttcgagtaga gaattgccga catcaacctc	60
31 catgttctcg gccgtaagga acttaccctt gctgagaagg aaatgccagg tcttatgggt	120
32 cttcgtgagc gttattccgc ttctaagcca ttgaagggtg tcagaatctc tggttccctc	180
33 cacatgacag tccagacagc cgtcctcatc gagacactca cagctcttgg tgctgatgtc	240
34 agatgggctt cctgcaacat cttctctaca caagatacag ccgctgctgc tatcgttgct	300
35 ggccaacag gcacaccaga gaagccagcc ggtatcccag tcttcgcctg gaaggcgaa	360
36 aactcccag aatactggga gaacacatac cgcgctctca catggccaga tggtaaggc	420
37 ccacagcagg ttgtcgatga tgggtggtgat gctacactcc tcacttccaa gggcttcgaa	480
38 ttcgaaacag ccggtgctgt tccagagcca acagaagctg acaacctcga ataccgtgc	540
39 gttcttgcta cactcaagca ggtcttcaac caagacaaga accactggca cacagttgct	600
40 gccggcatga acggtgtttc cgaagagaca acaacagggtg tccaccgcct ctaccagtc	660
41 gagaaggagg gcaaactcct cttcccagcc atcaacgtca acgacgtgt taaaaagtc	720
42 aagttcgata acatctacgg ctgccgccac tcccttatcg atggtatcaa ccgtgcttcc	780
43 gatgtcatga tcggcggcaa gacagctctc gtcattgggt acggcgatgt cggcaagggc	840
44 tgcgtcaat ccctccgtgg ccaaggcgtc cgcgttatca tcacagaact cgaccaatc	900
45 tgcgtctctc aggtgccat ggaaggctac caggtccgcc gcatcgagga agtcgtcaag	960
46 gatgtcgata tcttcgttac atgcacagga aactgcgata tcactctctg tgacatgatg	1020
47 gccagatga aggataaggc tattgtcggg aacatcggcc acttcgataa cgaaattgat	1080
48 acagatggcc tcattgaaata cccaggcatc aagcacatcc caatcaagcc agaatacgac	1140
49 atgtgggaat tccagatgg ccacgctatc ctcttcttg ctgagggcgg ccttcttaac	1200
50 cttggtctgc ctacaggtca cccatctttc gttatgtcaa tgtcattcac aaaccagaca	1260
51 ctgcctcagc tcgacctcta cgaaaagaga ggaaatctcg agaagaagg ttacacactt	1320
52 ccgaagcatc tcgatgaaga agtcgctcgc ctccacctcg gatctctcga tgtccacctt	1380
53 acaaagctta cacagaagca ggctgactac atcaacgttc cagttgaggg tccttacaag	1440
54 tctgatgctt accgttatta a	1461

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58 <210> SEQ ID NO: 2
59 <211> LENGTH: 33
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Upstream primer
66 <400> SEQUENCE: 2
67 ttttgatcc gcttgcaaata cacctgctgg tgc 33
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 24
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Downstream pprimer
78 <400> SEQUENCE: 3
79 ttttctgcag ggggagctat cgct 24
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 38
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: Primer
89 <400> SEQUENCE: 4
90 catcatcatc atcatcacgc ttgcaaata cctactgg 38
93 <210> SEQ ID NO: 5
94 <211> LENGTH: 30
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Primer
101 <400> SEQUENCE: 5
102 ctacgaatgg caataattcc taggtacgta 30
105 <210> SEQ ID NO: 6
106 <211> LENGTH: 1461
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens (nucleotide sequence of SAHH - wild type)
110 <400> SEQUENCE: 6
111 atggcttgca aatcacctgc tgggtgctcca ttcgagtaca gaattgccga catcaacctc 60
112 catgttctcg gccgtaagga acttaccctt gctgagaagg aaatgccagg tcttatggtt 120
113 cttcgtgagc gttattccgc ttctaagcca ttgaagggtg tcagaatetc tggttccctc 180
114 cacatgacag tccagacagc ggtccttatt gagacactca cagctcttgg tgctgatgtc 240
115 agatgggctt cctgcaacat cttctctaca caagatacag ccgctgctgc tatcgttgtc 300
116 ggcccaacag gcacaccaga gaagccagcc ggtatcccag tcttcgcctg gaagggcgaa 360
117 aactccag aatactggga gaacacatac cgcgtctcga catggccaga tggtaaggc 420
118 ccacagcagg ttgtcgatga tgggtggtgat gctacactcc tcatctccaa gggcttcgaa 480
119 ttcgaaacag ccggtgctgt cccagagcca acagaagctg acaacctcga ataccgctgc 540
120 gttcttgcta cactcaagca ggtcttcaac caagacaaga accactggca cacagttgct 600
121 gccggcatga acggtgtttc cgaagagaca acaacaggtg tccaccgcct ctaccagctc 660
122 gagaaggagg gcaaactcct cttccagacc atcaacgtca acgacgctgt taaaaagtc 720

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123 aagttcgata acatctacgg ctgtcgccac tcccttatcg atggtatcaa ccgtgcttcc      780
124 gatgtcatga tcggcggaac gacagctctc gtcatgggtt acggcgatgt cgggaagggc      840
125 tgcgctcaat ccctccgtgg ccaaggcgct cgcgttatca tcacagaact cgaccctatc      900
126 tgcgctctcc aggctgtcat ggaaggctac caggctcgcc gcatcgagga agtcgtcaag      960
127 gatgtcgata tcttcgttac atgcacagga aactgcgata tcatctctgt tgacatgatg     1020
128 gccagatga aggataaggc tattgtcggg aacatcggcc acttcgataa cgaaattgat     1080
129 acagatggcc tcatgaaata ccaggcatc aagcacatcc caatcaagcc agaatacgac     1140
130 atgtgggaat tcccagatgg ccacgctatc ctcttcttct ctgagggccg ccttcttaac     1200
131 cttggttgcg ctacaggtea cccatctttc gttatgtcaa tgtcattcac aaaccagaca     1260
132 ctgcgtcagc tcgacctcta cgaaaagaga ggaaatctcg agatgaaggt ttacacactt     1320
133 ccgaagcatc tcgatgaaga agtcgttcgc ctccacctcg gatctctcga tgtccacctt     1380
134 acaaagctta cacagaagca ggctgactac atcaacgttc cagttgaggg tccttacaag     1440
135 tctgatgctt accgttatta a                                     1461
138 <210> SEQ ID NO: 7
139 <211> LENGTH: 486
140 <212> TYPE: PRT
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 7
144 Met Ala Cys Lys Ser Pro Thr Gly Ala Pro Phe Glu Tyr Arg Ile Ala
145 1 5 10 15
146 Asp Ile Asn Leu His Val Leu Gly Arg Lys Glu Leu Thr Leu Ala Glu
147 20 25 30
148 Lys Glu Met Pro Gly Leu Met Val Leu Arg Glu Arg Tyr Ser Ala Ser
149 35 40 45
150 Lys Pro Leu Lys Gly Val Arg Ile Ser Gly Ser Leu His Met Thr Val
151 50 55 60
152 Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Asp Val
153 65 70 75 80
154 Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln Asp Thr Ala Ala Ala
155 85 90 95
156 Ala Ile Val Val Gly Pro Thr Gly Thr Pro Glu Lys Pro Ala Gly Ile
157 100 105 110
158 Pro Val Phe Ala Trp Lys Gly Glu Thr Leu Pro Glu Tyr Trp Glu Asn
159 115 120 125
160 Thr Tyr Arg Ala Leu Thr Trp Pro Asp Gly Gln Gly Pro Gln Gln Val
161 130 135 140
162 Val Asp Asp Gly Gly Asp Ala Thr Leu Leu Ile Ser Lys Gly Phe Glu
163 145 150 155 160
164 Phe Glu Thr Ala Gly Ala Val Pro Glu Pro Thr Glu Ala Asp Asn Leu
165 165 170 175
166 Glu Tyr Arg Cys Val Leu Ala Thr Leu Lys Gln Val Phe Asn Gln Asp
167 180 185 190
168 Lys Asn His Trp His Thr Val Ala Ala Gly Met Asn Gly Val Ser Glu
169 195 200 205
170 Glu Thr Thr Thr Gly Val His Arg Leu Tyr Gln Leu Glu Lys Glu Gly
171 210 215 220
172 Lys Leu Leu Phe Pro Ala Ile Asn Val Asn Asp Ala Val Thr Lys Ser
173 225 230 235 240
174 Lys Phe Asp Asn Ile Tyr Gly Cys Arg His Ser Leu Ile Asp Gly Ile

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175		245		250		255
176	Asn Arg Ala Ser Asp Val Met Ile Gly Gly Lys Thr Ala Leu Val Met					
177		260		265		270
178	Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Gln Ser Leu Arg Gly Gln					
179		275		280		285
180	Gly Ala Arg Val Ile Ile Thr Glu Leu Asp Pro Ile Cys Ala Leu Gln					
181		290		295		300
182	Ala Ala Met Glu Gly Tyr Gln Val Arg Arg Ile Glu Glu Val Val Lys					
183	305		310		315	320
184	Asp Val Asp Ile Phe Val Thr Cys Thr Gly Asn Cys Asp Ile Ile Ser					
185		325		330		335
186	Val Asp Met Met Ala Gln Met Lys Asp Lys Ala Ile Val Gly Asn Ile					
187		340		345		350
188	Gly His Phe Asp Asn Glu Ile Asp Thr Asp Gly Leu Met Lys Tyr Pro					
189		355		360		365
190	Gly Ile Lys His Ile Pro Ile Lys Pro Glu Tyr Asp Met Trp Glu Phe					
191		370		375		380
192	Pro Asp Gly His Ala Ile Leu Leu Leu Ala Glu Gly Arg Leu Leu Asn					
193	385		390		395	400
194	Leu Gly Cys Ala Thr Gly His Pro Ser Phe Val Met Ser Met Ser Phe					
195		405		410		415
196	Thr Asn Gln Thr Leu Ala Gln Leu Asp Leu Tyr Glu Lys Arg Gly Asn					
197		420		425		430
198	Leu Glu Lys Lys Val Tyr Thr Leu Pro Lys His Leu Asp Glu Glu Val					
199		435		440		445
200	Ala Arg Leu His Leu Gly Ser Leu Asp Val His Leu Thr Lys Leu Thr					
201		450		455		460
202	Gln Lys Gln Ala Asp Tyr Ile Asn Val Pro Val Glu Gly Pro Tyr Lys					
203	465		470		475	480
204	Ser Asp Ala Tyr Arg Tyr					
205		485				

VERIFICATION SUMMARY

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